

query	LVAFADFG-SVTFTNAEATSGGSTVGPSDATVMDIEQDGSVLTTETSVSGDS-VTV
sequence1	LVAFADFG-SVTFTNAEATSGGSTVGPSDATVMDIEQDGSVLTTETSVSGDS-VTV
sequence2	LVPFANFG-TVTFTGAEATTSSGTVTAADATLIDIEQNGEVLTSVTVSGST-VTV
sequence3	LVQFANFG-TVTFTGASATQNGESVGVTGAQIIDLQQN-SVLTSVSTSNS-VTV
sequence4	LVNFADF-TVTFKDCSPSVSG-----STIVDIRQSLEVLTECSTTGTTTVTC
sequence5	FVPFASFSPAVEFTDCSVTSDGESVSLDDAQITQVIINNQDVTDCSVSGTT-VSC
sequence6	FVPFASFSPAVEFTDCSVTSDGESVSLDDAQITQVIINNQDVTDCSVSGTT-VSC
sequence7	FVPFASFSPAVEFTDCSVTSDGESVSLDDAQITQVIINNQDVTDCSVSGTT-VSC

FIGURE 1

SECRET

	B	I	G	T	O	W	N	S	O	W	N
B	2										
I		2									
G			2								
B	2										
R											
O					2				2		
W						2				2	
N							2				2
T				2							
O					2				2		
W						2				2	
N							2				2
O					2				2		
W						2				2	
N							2				2

FIGURE 2.

	B	I	G	T	O	W	N	S	O	W	N
B	2										
I		2									
G			2								
B	2										
R											
O					2				2		
W						2				2	
N							2				2
T				2							
O					2				2		
W						2				2	
N							2				2
O					2				6	0	0
W	0	0	0	0	0	4	0	0	0	4	0
N	0	0	0	0	0	0	2	0	0	0	2

FIGURE 3.

FOUO-925060

FIGURE 4.

	B	I	G	T	O	W	N	S	O	W	N
B											
I											
G											
B											
R											
O											
W					0	2	3	4	5	6	7
N					2						
T					3						
O					4						
W					5						
N					6						
O					7						
W					8						
N					9						

FIGURE 5.

FIGURE 5 - 041200

	B	I	G	T	O	W	N	S	O	W	N
B	16	10	8	7	4	3	2	1	0	0	0
I	12	14	9	8	6	4	3	2	0	0	0
G	10	12	12	9	6	6	4	3	0	0	0
B	10	10	12	10	7	4	6	4	1	0	0
R	10	9	10	12	8	5	4	6	2	0	0
O	12	10	9	8	12	6	3	2	6	0	0
W	10	12	10	7	6	10	4	3	0	4	0
N	9	10	12	8	5	4	8	4	1	0	2
T	6	7	8	12	6	4	4	6	2	0	0
O	4	6	5	6	10	6	4	3	6	0	0
W	3	4	6	4	4	8	6	4	1	4	0
N	2	3	4	6	2	3	6	6	2	0	2
O	0	0	1	2	6	0	1	2	6	0	0
W	0	0	0	0	0	4	0	0	0	4	0
N	0	0	0	0	0	0	2	0	0	0	2

FIGURE 6.

00005176-071204
TOTAL 20 " 92T50050

FIGURE 7

BIG-TOWNSOWN---

BIGBROWNTOWNOWN Similarity = 18. Gap = -2. Total Score = 16

09605476-074204
F02E40-92F50660

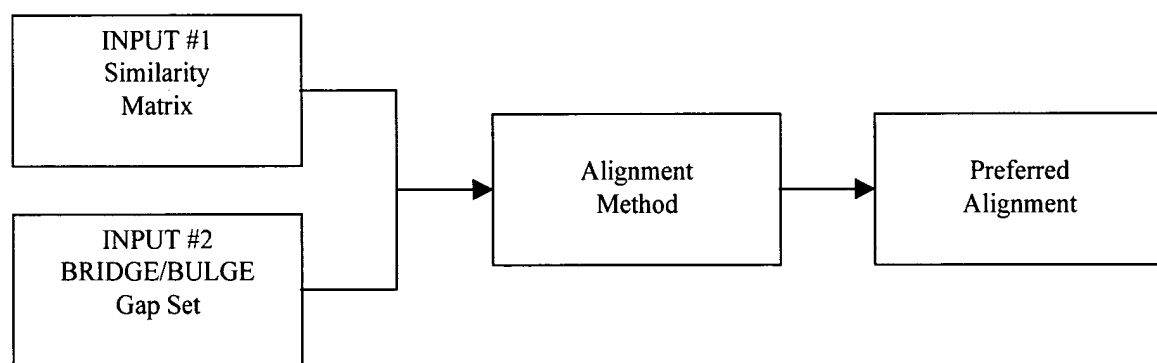


FIGURE 8

0905476-074201

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Gap Type	Start Res.	End Res.	# Residues
BULGE	3 (G)	5 (O)	7
BRIDGE	7 (N)	9 (O)	1

FIGURE 9.

FOOTNOTES: 9250600

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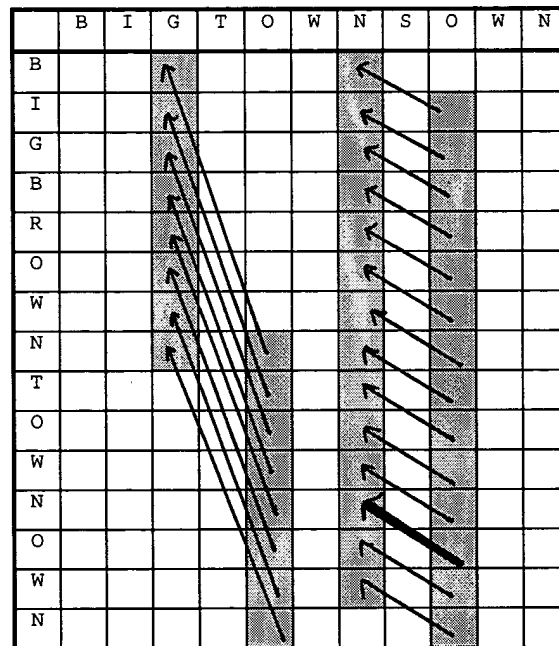


FIGURE 10

[illegible]

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	B	I	G	T	O	W	N	S	O	W	N
B	2										
I		2									
G			2								
B	2										
R											
O					2				2		
W						2				2	
N							2				2
T				2							
O					2				2		
W						2				2	
N							7	6	1	0	2
O	0	0	0	1	6	0	0	1	6	0	0
W	0	0	0	0	0	4	0	0	0	4	0
N	0	0	0	0	0	0	2	0	0	0	2

FIGURE 11.

[illegible]

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	B	I	G	T	O	W	N	S	O	W	N
B	2										
I		2									
G			12	7	5	6	3	0	0	0	0
B	7	9	12	9	2	5	6	3	0	0	0
R	8	6	5	12	5	1	5	6	1	0	0
O	11	8	6	5	12	5	1	1	6	0	0
W	8	11	8	3	5	10	3	0	0	4	0
N	6	8	11	8	3	5	8	3	0	0	2
T	6	6	8	11	6	3	5	6	1	0	0
O	3	6	3	6	11	6	3	1	6	0	0
W	1	3	6	3	4	9	6	3	0	4	0
N	0	1	3	6	1	1	7	6	1	0	2
O	0	0	0	1	6	0	0	1	6	0	0
W	0	0	0	0	0	4	0	0	0	4	0
N	0	0	0	0	0	0	2	0	0	0	2

FIGURE 12

FOR 20" 94T50050

Deditions

	B	I	G	T	O	W	N	S	O	W	N
B											
I											
G											
B				0	3	5	7	9	11	13	15
R				3							
O				5							
W				7							
N				9							
T				11							
O				13	1						
W				15							
N				17							
O				19							
W				21							
N				23							

FIGURE 13

FIGURE 14.

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FIGURE 15

BIG-----TOWNSOWN

BIGBROWNT-OWN-OWN Sim. = 18. Gap = -2. Total Score = 16.

000545-074201
FOET20-92T50000

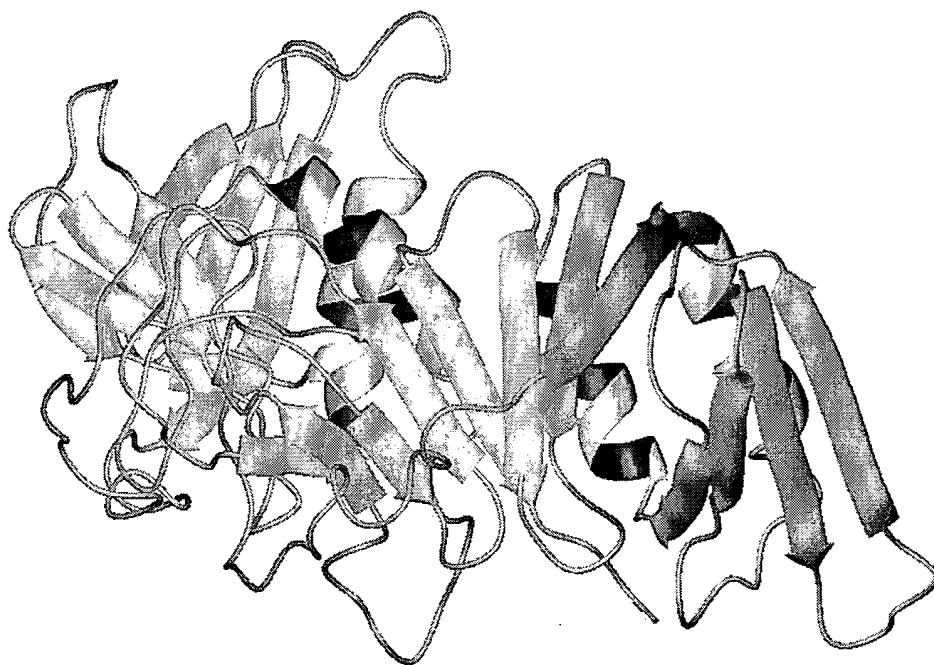


FIGURE 16

102F20-92T50660

>P1;1b4k

```
structureX:1b4k: 10 :A : 335 :A :
```

YPYTRLRRNRDDFSRRLVRENVLTVDDLILPVFVL DGVNQRESIPSM PGVERLSIDQLLIEAE
EWVALGIPALALFPVT:PVEKKSLDAAEAYNPEGIAQRATRALRERFPELGIITDVALDPFTTH
GQDGILDDDDGYVLNDVSI DVLVRQALSHAEAGA QVVAPSDMMDGRIGAI REALESAG:HTNVR I
MAYSAKYASAYYGPF RDAVG SASNLGKG NKATYQMDPANSDEALHEVAADLAEGADMVMVKPGM
PYLDIVRRVK:DEFRAPTFVYQVS GEYAMHMGAIQNGWLAE:SVILESLTAFKRAGADGILTYF
AKOAAEOLRR*

>P1;SC001

```
sequence:SC001: 13 : : 340 :
```

sequence: 35001: 15 : 4 : 310 :
EISSVLAGGYNHPLLQWQSERQLTKNMLIFPLFISDNPDDFTEIDSLPNINRIGVNRCLKDYLK
PLVAKGLRSVILFGVPLIPGTKDPVGTAADDPAGPVIQGIKFIREYFPELYIICDVCLCEYTSH
GHCGVLYDDGTINRERSVSRLLAAVAVNYAKAGAHCVAPSDMIDGRIRDIKRGLINANLAHKTFV
LSYAAKFSGNLYGPFDAACSA: :PSNGDRKCYQLPPAGRGLARRALERDMSEGADGIIVKPS
FYLDIMRDASEICKDLPICAHYVSGEYAMLHAAAEGVVDLKTIAFESHQGLRAGARLIITYL
APEFLDWLDE*

FIGURE 17

THE

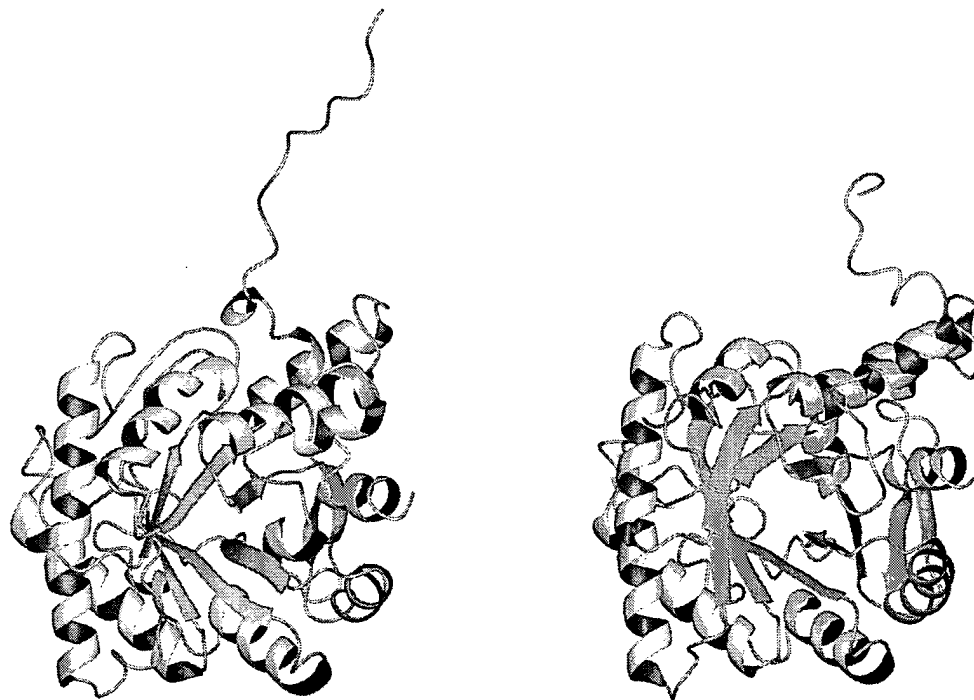


FIGURE 18

00005176-074204

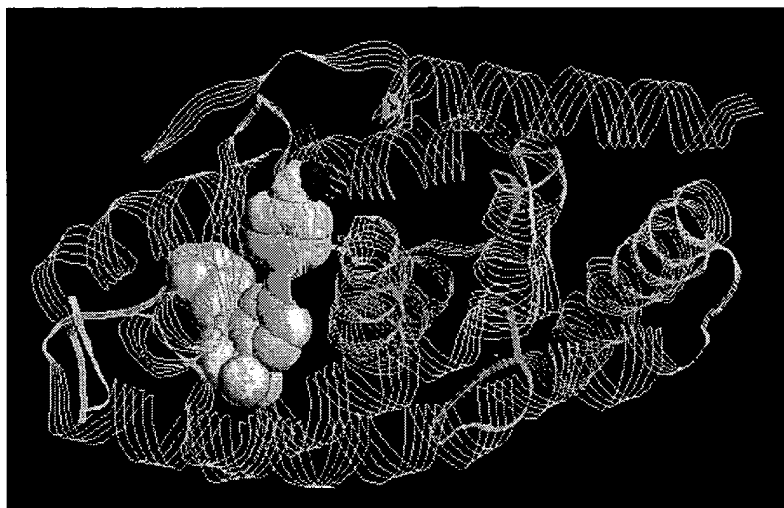


FIGURE 19

FIGURE 19

>P1;1a28
structureX: 1a28A : 701 : : 915 : :
AGHDNTKPDTSSTSLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDDQITLIQYSWMSLMVFGWGWSYKHVS
GQMLYFAPDLILNEQRMKESSFYSLCLTMW-QIPQEFVKLQVSQEEFLCMKVLLLLNTI-PLEGLRSQTQFE
EMRSSYIRELIKAIGLRQKGVVSSSRFYQLTKLLDNLHDLVKQLHLYCLNTFIQSRALSVEFPMMSEVIA
A*
>P1;gi7766906
sequence: gi7766906 : 27 : : 233 :
EANMGLNPSSPNDPVTNICQAADKQLFTLVEWAKRIPHFSELPLDDQVILLRAGWNELLIASASHRSIA--V
KDGILLATGLHVHRNSAHSAGVGAI FDRVLTTELVS KM RDMQMDKTELGCLRAIVLFNPDS--KGLSNPAEVE
ALREKVYASLEAYCKHKYP---EQPGRFAKLLRLPALRSIGLKCLEHLFF-FKLIGDT--PIDTFLMEMLE
A*

FIGURE 20

090515-07404

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FIGURE 21

090517-0342
T02T00-9ZT50660

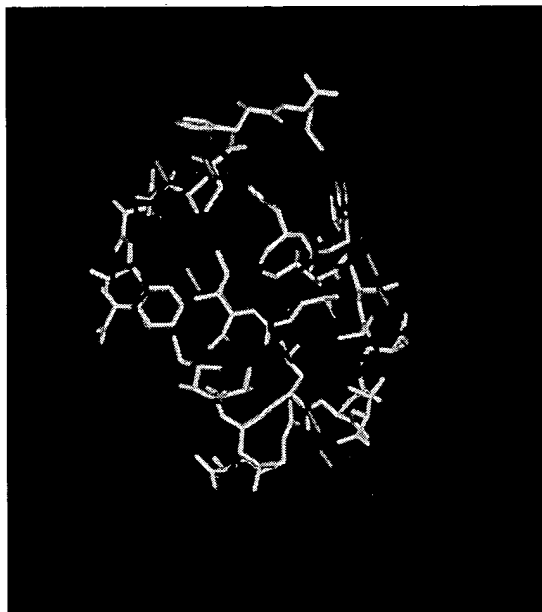
[illegible]

FIGURE 22

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SECRET

>P1;1a28
structureX: 1a28A : 682 : : 921 : :
QLIPPLINLLMSIEPDVIYAGHDNTKPDTS S S L L T S L N Q L G E R Q L L S V V K W S K S L P G F R N L H I D D Q I T L I Q Y
S W M S L M V F G L G W R S Y K H V S G Q M L Y F A P D L I L N E Q R M K E - S S F Y S L C L T M W Q I P Q E F V K L Q V S Q E E F L C M K V L
L L L N - - - - T I P L E G L R - - - S Q T Q F E E M R S S Y I R E L I K A I G L R Q K G V V S S S Q R F Y Q L T K L L D N L H D L V K Q L H L
Y C L N T F I Q S R A L S V E F P E M M S E V I A A Q L P K I L *
sequence: gi3659931 : 14 : : 254 :
L T A D Q M V S A L L D A E P P I L Y S E Y D P T R P F S E A S M M G L L T N L A D R E L V H M I N W A K R V P G F V D L T L H D Q V H L L E C
A W L E I L M I G L V W R S M E H P - - G K L L F A P N L L L D R N Q G K C V E G M V E I F D M L L A T S S R F R M M N L Q G E E F V C L K S I
I L L N S G V Y T F L S S T L K S L E E K D H I H R V L D K I T D T L I H L M A K A G L T L Q Q H E R L A Q L L L I L S H I R H M S N K G M E
H L Y S M K C K N - - - V V P L Y D L L L E M L D - A H R - L H *

FIGURE 24

FIGURE 24 = 92150060



FIGURE 25

09905476-074204

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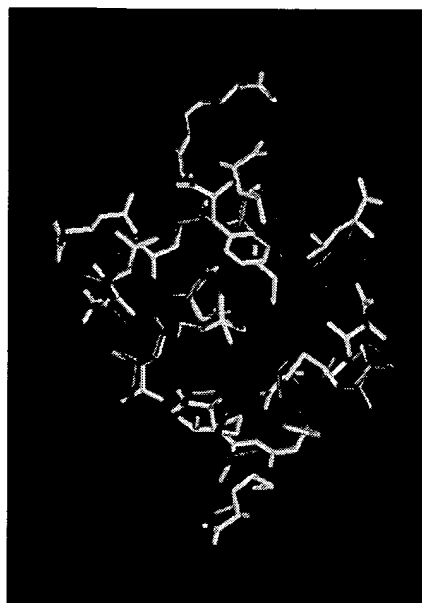


FIGURE 26

090516-071201
T02F20-S2F50660

```
>P1;1c3w
structureX: 1c3wA :    5 :    : 231 :
TGRPEWIWLALGTALMGLGTLTYFLVKGMGVSDPDACKFYAITTLVPAIAFTMYLSMLLGYLTMVPFGGE--
QN-- --PIYW-ARYADWLFTFTPLLLDLALLVDADQGTILALVGADGIMIGTGLVGALTKEY--S--YRFVW
WAISTA-AMLYILYLVLFGG- ----SMRPE-VA-STFKVLRLNVTVVLWSAYPVVWLIGSEG----AGI---V
PLNIETLLFMVL-DVSAKVGFGLLILRSRAIFG*

>P1;1e12A
sequence: 1e12A :    4 :    : 236 :
ENALLSSSLVNVALAGIAILVFVYMGRTIRPGRPLIWGATLMIPLVSISSYLGLLSGLTVGMIEMPAGHA
LAGEMVRSQW-GRYLTWALSTPMILLALGLLADVDLGSFLTIVAADIGMCVTGLAAAMTTS-- --ALLFRWAF
YAISCA-FFVVVLSALVTDWAASASAGT- -A--EIFDTRLVLTVVLWLGYPIVWAVGV-----EGLALVQ
SVGATSWAYSVL-DVFAKYVFVAFILLRWVANNE*
```

FIGURE 27

DECLASSIFICATION

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FIGURE 28

FOOT 20-5450560

FSMLAAYMPELLIMLGFPINFLTVTVQHKKLRT----PLNYILLNLAVADLFMVGFGFTTTLYTSLHGYP
VFGPTGCNLEGFFATLGGGEIALWSLVLAIERVYVVCCKPMSNFRFGENHAIMGVAFTWVMALACAAPLVGW
SRYIPEGMQCSGIDYYTPHEETNNESFVIYMFVVHFIIPLIVIFFCYGQLVFTV-KEAASATTQKAEKEV
TRMVIIMVIAFLICWLPYAGVAFYIFTHOGSDFGPIMFTIPAFFAKTSAVYNPVIYIM*

>P1;1c3wA

```
sequence: 1c3wA : 2 : 215 : GRPEWIWLALGTALMGLGTLTYFLVKGMGVSDPDAKKFYA-
ITTLVPAIAFTMYLSMLLGYGTLMPV-FGGEQ
--NPI-YWARYADWLFTTPLLLLDLALLVDA-----D-----QGTILALVGADGIMIGTGLVGAL----
TKVY-----SY-----RfvvwaIstAAMLYILYLVFFGFsMR--PEV-----ASTfKVL
RNVTVVLWSAYpVVVLIGSEGAGI-----VPLNI--ETTLfMVLdVSAKVGfGLIL*
```

FIGURE 29

[illegible]

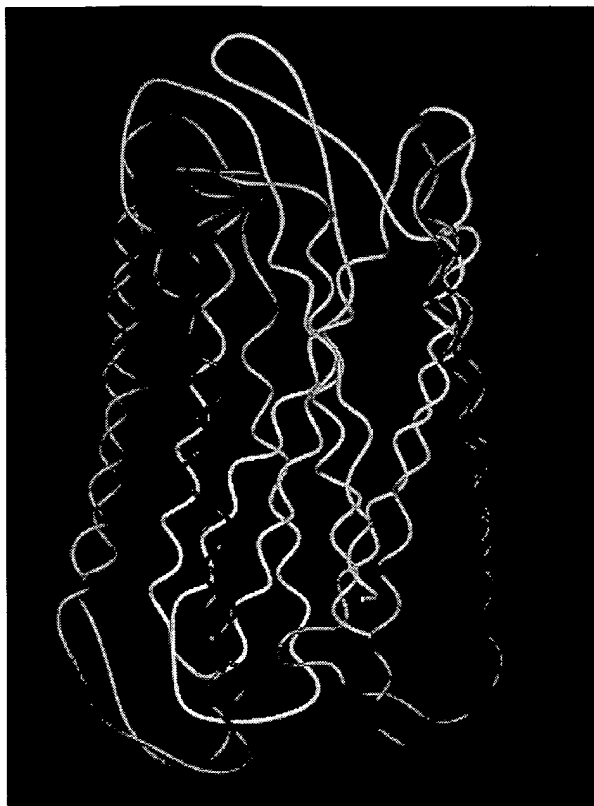


FIGURE 30

00005176-071201
T02T20-92T50660

>P1;6prc
structureX: 6prcL : 14 : : 258 : : GTLIGGDLFDWVGPYFVGFFGVSAIFFIFLGVSLIGYAASQG-P----
---TW-DPFAISINPPDLKYGLG
A-APLLEGGFWQAITVCALGAFISWMLREVEISRKLIGWHVPLAFCVPIFMFCVLQVFRPLLGSWGHAFF
YGILSHLDWVNNFGYQYLNWHYNPGHMSSVSFLFVNAMALGLHGGLILSVANP-GD----GD-----
-KVKTA-EHENQYFRDVVGYSIGALSIHRLGLFLASNIFLTGAFTIASGPFWTRG*
>P1;6prcM
sequence: 6prcM : 34 : : 292 :
YSYWLKIGDAQIGPIYLGASGIAAFAGSTAILIILFNMAAEVHFDPLQFFR--QFFWLGLYPPKAQYGMG
I-PPLHDGGWWMAGLFMTLSLGSWWIRVYSRARALGLGTHIAWNFAAAIFFVLCIGCIHPTLVGSWSEGVP
FGIWPIDWLTAFSIRYGNFYPCWHGFSIGFAYGCGLLFAAHGATILAVARFG-----GDREIEQITDRG
T--AV--ERAALFWRWTIGFNATIESVHRGWFFSLMVMVSASVGILLTGTFVDNW*

FIGURE 31

0905175-071204

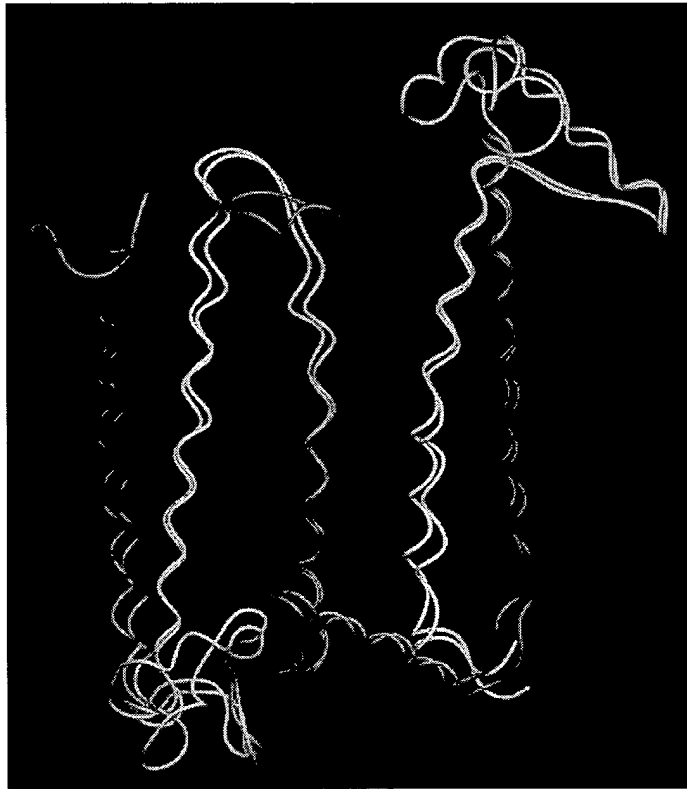


FIGURE 32

>P1;1qj8
structureX: 1qj8A : 4 : : 148 : :
TVTGGYAQSDAQGM-NKMGGFNLKYRYEEDNSPLGVIGSFTYTE-K--SRTASSGDYN-KNQYYGITAGPA
YRINDWASIYGVVGVGYGKFTTEYPTYK-NDTSDYGFSYGAGLQFNPMENVALDFSYEQSRIRS-----
--VDVGTWIAGVGYRF*
>P1;1bxwA
sequence: 1bxwA : 19 : : 171 :
YHDTGLINNN--GPTHENKLGAGAFGGYQV-NPYVGFEMGYDWL--GRMPYKGSVENGAYKAQGVQLTAKLG
YPITDDLDIYTRLGGMVWRADTY-SNVYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGT
RP-DNGMLSLGVSYRF*

FIGURE 33

TOET 40 94T50000

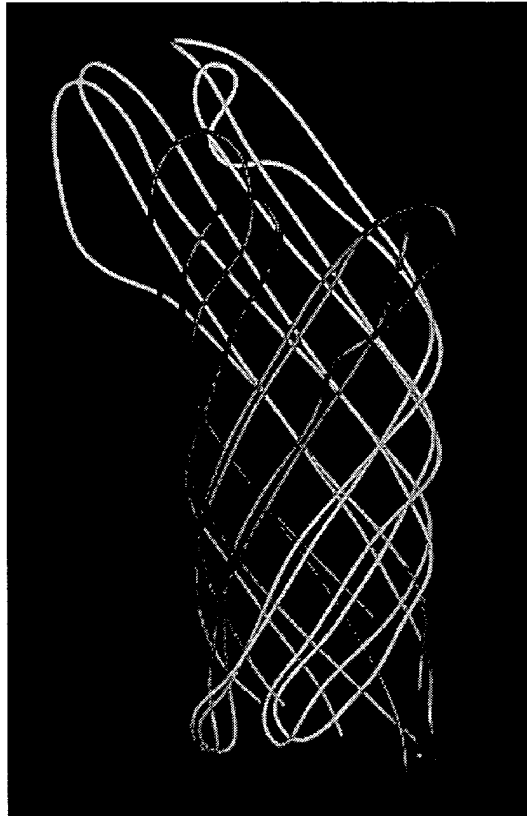


FIGURE 34

0005176-0701
T02T40-92T50660

FIGURE 35

bioRxiv preprint doi: <https://doi.org/10.1101/067897>; this version posted May 10, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

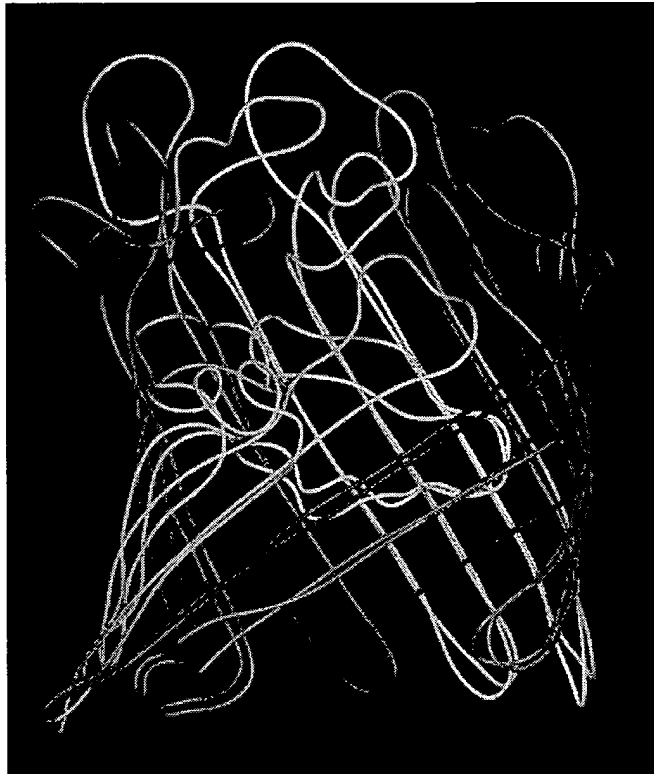


FIGURE 36

TOP SECRET

P1;2mpr
structureX: 2mprA : 2 : : 427 : :
DFHGYARSGIGWTGS-----G---GEQQC-----FQA--TGAQSKYRLGNE-----
--CETYAELKLGQEVWKEGDKSFYFDTNVAYSVNQQND--WEST-DPAFREANVQGKNL---IEWLPGSTIW
AGKRFYQRHD---VHMIDFYYWDISGPGAGIENIDLGFGLS-LAATRSTEAGGSYTFSSQNIYDEVKDTAN
DVFDVRLAGLQTNPDGVLELGVLDYGRANTTDGYKL-ADGASKDGWMFTAHTQSMLKGYNKFVVQYATDAMT
TQKGQARGSDGSSSFTEKINYANKVINNNG-NMWRILDHGAISLGDKWDLMYVGMYNIDWDNNL--GTEW
WTVGVPRPMYKWTPI MSTLLEVGYDNVKS-QQ-----TGDRNNQYKITLA-QQ---WQAGDSIWSRPAIRI
FATYAKWDEKGYIKDGNISRYAAAT-NSGISTNSRGDSDEWTFGAQMEIWW*
>P1;1a0tP
sequence: 1a0tP : 4 : : 413 : :
EFHGYARSGVIMNDGASTKSGAYITPAGETGG-----AIGRL-----GNQ-----
--ADTYVEMNLEHKQTLN GATTRFKVMVADGQTSYNDWTASTS-DLNVRQAFVELGNLPTFAGPFGSTLW
AGKRF--DRDNFDIHWIDSDVVFLAGTGGGIYDVKNWDLRSNFSLYGRNFGDIDDSSNSVQNYILTMNHFA
GPLQMMVSGLRKDNDRKDSNG-NLAKGDAANTGV----HALLGLHNSFYGLRDGSSKTALLYG-HGLG
AEVKGIGSDGA-----LRPGADTWRIASYGTTPLSENWSVAPAMLAQRSKDRYADGDSYQW
ATFNLRLIQAINQN FALAYEGSYQYMD--LKPEGYNDRQAVNGSFYKLTF--APTFKVGSI GDFFSRPEIRF
YTSWMDWSKKLNNYASDDALGS---DGF-----NSGGEWSFGVQMETWF*

FIGURE 37

FIGURE 37



FIGURE 38

FOOT 40-92T50000